

Docket No. CL001181DIV2
Serial No. To Be Assigned
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEINS...

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1 TGGAGGAGCC AGCGGAAGGA CGGTGTGCGG GCCGGCCAGC CCTGGACGAA
51 AGAAGAGGGC CCTCCAGGC CAGTCTGGGC ACCCTGGGAT AGCGGCTGCA
101 GCCAGGCATG GCCGACTCTG CACAGGCCCA GAAGCTGGTG TACCTGGTCA
151 CAGGGGGCTG TGGCTTCCTG GGAGAGCACG TGGTGCGAAT GCTGCTGCAG
201 CGGGAGCCCC GGCTCGGGGA GCTGCGGGTC TTTGACCAAC ACCTGGGTCC
251 CTGGCTGGAG GAGCTGAAGA CAGGTACCCG GAACGTGATC GAGGCTTGTTG
301 TGCAGACCGG AACACGGTTC CTGGTCTACA CCAGCAGCAT GGAAGTTGTG
351 GGGCCTAACA CCAAAGGTCA CCCCTTCTAC AGGGGCAACG AAGACACCCC
401 ATACGAAGCA GTGCACAGGC ACCCCTATCC TTGCAGCAAG GCCCTGGCCG
451 AGTGGCTGGT CCTGGAGGCC AACGGGAGGA AGGTCCGTGG GGGGCTGCCC
501 CTGGTGACGT GTGCCCTTCG TCCCACGGGC ATCTACGGTG AAGGCCACCA
551 GATCATGAGG GACTTCTACC GCCAGGGCCT GCGCCTGGGA GGTGCGCTCT
601 TCCGGGCCAT CCCGGCCTCT GTGGAGCATG GCCGGGTCTA TGTGGCAAT
651 GTTGCTTGA TGCAGTGCT GGCAGCCCG GAGCTGGAGC AGCGGGCAGC
701 CCTGATGGGC GGCCAGGTAT ACTTCTGCTA CGATGGATCA CCCTACAGGA
751 GCTACGAGGA TTTCAACATG GAGTTCCTGG GCCCTGCGG ACTGCGGCTG
801 GTGGGCGCCC GCCCATTGCT GCCCTACTGG CTGCTGGTGT TCCTGGCTGC
851 CCTCAATGCC CTGCTGCAGT GGCTGTGCG GCCACTGGTG CTCTACGCAC
901 CCCTGTGTGA CCCCTACACG CTGGCCGTGG CCAACACCAC TTCCACCGTC
951 AGCACCGACA AGGCTCAGCG CCATTTTCGGC TATGAGCCCC TGTCTCGTG
1001 GGAGGATAGC CGGACCCGCA CCATTCTCTG GGTACAGGCC GCTACGGGTT
1051 CAGCCCAGTG ACGGTGGGGC TGGGGCCTGG AGGCCCAGAT ACAGCACATC
1101 CACCAGGTC CCGAGCCCTC ACACCCTGGA CGGGAAGGGA CAGCTGCATT
1151 CCAGAGCAGG AGGACAGGGCT CTGGGGCCAG AATGGCTGTC CTTGTCGTAG
1201 AGCCCTCCAC ATTTTCTTTT TCTTTTGA GACAGGCTCT TGCTCTGTCA
1251 CCCAGACTGG AGTGCACTGG TGTGATCATA GCTCACTGCA CCCTCAACCT
1301 CCTGGGTTCA AGCAATCCTC CTGCCTCAGC CTCCTGAACA GCTGGGACCA
1351 CAGGTGCACG CCACCATAAC TGGCTTTTTT TTGTTGCTTT TAGAGACAGG
1401 GTCTCACTAT ATTGCTCAAG GCTGGACTTG AACTCCTGGG CTCAAGTGAT
1451 CTTCCACAGT GGGCCTCCCA AAACGCTGGA ACTACAAGTG TGAGCCACCG
1501 CGCCTGGCCC ACCGCCTCTC CACATTTTCA ATCCAGGAGC CTTGAGTCTG
1551 TGGCTGTGTC GTGACACCTC CAGAGTTCTG AGGGCCGTCA GGACACGGGA
1601 GGGTTTGGGG ACAGAGTGTC CTTCTCTGT CCTATCATCA CCAGTCTGA
1651 TGGCCGCTTG GTGAGTGCT GGTGCCCTGG TGGCTTGCCC CAGCTCTCTT
1701 GTGGCTTTCT GAGCAGGAAG CGAGCACTAG GCTCCACAGG CTTACGCTGT
1751 GTCTCTGCC AGCCACACAG CGACCCATCG GTGCAGAGTG CAGACGCGGG
1801 TGTGTTCTCT CCAGCCCACC TCAGTCCCTC TTTGGGAGGT GATGTTCCCA
1851 TTGTTTTC AAGGCCTCAC CTTCAACTGT TCTGTTTAG AATTCCCCTC
1901 TGGAGGGCTA TGGCCTCCCT ATGGTTTCAC TTCCACCTA CTTCTACCTA
1951 AGTTCCTTCC CAGCACATCG CCAGCCCTGG GCCTGGGGAT GTCCCAATG
2001 CTGTACCTGG CTGACCCCGG ATTAAAGCC TCATCCACGA AAAAAAAAAA
2051 AAAAAAAAAA AAAAAAAAAA A

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(SEQ ID NO: 1)

FEATURES:

5'UTR: 1-107
Start Codon: 108
Stop Codon: 1059
3'UTR: 1062

HOMOLOGOUS PROTEINS:

Top 10 BLAST Hits:

CRA 335001098696094 /altid=gi 11545403 /def=gb AAG37824.1 AF277...	638	0.0
CRA 335001098696092 /altid=gi 11545401 /def=gb AAG37823.1 AF277...	562	e-159
CRA 18000005106837 /altid=gi 2563999 /def=dbj BAA22931.1 (AB00...	484	e-136
CRA 18000005043125 /altid=gi 9629084 /def=ref NP_044103.1 MC15...	269	3e-71
CRA 89000000192042 /altid=gi 9634716 /def=ref NP_039008.1 ORF ...	257	2e-67
CRA 18000004899504 /altid=gi 540666 /def=pir S41971 3beta-hydr...	240	1e-62
CRA 335001098644340 /altid=gi 11251676 /def=pir T37430 hydroxy...	213	2e-54
CRA 18000004942649 /altid=gi 112779 /def=sp P26670 3BHS_VACCV 3...	212	4e-54

FIGURE 1A

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CRA 18000004942648	/altid=gi 9791111	/def=ref NP_063838.1	A44L...	211	9e-54
CRA 73000005493670	/altid=gi 9634564	/def=ref NP_038102.1	TA55...	211	9e-54

FIGURE 1B

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EST:

gi 11283574 /dataset=dbest /taxon=96...	1283	0.0
gi 11643588 /dataset=dbest /taxon=96...	1116	0.0
gi 13134586 /dataset=dbest /taxon=960...	527	e-147
gi 9334685 /dataset=dbest /taxon=960...	462	e-128

EXPRESSION INFORMATION FOR MODULATORY USE:

gi 11283574	brain
gi 11643588	kidney
gi 13134586	colon
gi 9334685	uterus

FIGURE 1C

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1 MADSAQAQKL VYLVGTGCGF LGEHVVRMLL QREPRLGELR VFDQHLGPWL
51 EELKTGTRNV IEACVQTGTR FLVYTSSMEV VGPNTKGHPF YRGNEPTPYE
101 AVHRHPYPCS KALAEWLVL EANGRKVRGGL PLVTCALRPT GIYGEHQIM
151 RDFYRQGLRL GGWLFRAIPA SVEHGRVYVG NVAWMHVLAA RELEQRAALM
201 GGQVYFCYDG SPYRSYEDFN MEFLGPCGLR LVGARPLLPY WLLVFLAALN
251 ALLQWLLRPL VLYAPLLNPY TLAVANTTFT VSTDKAQRHF GYEPLFSWED
301 SRTRTLWVQ AATGSAQ
(SEQ ID NO: 2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

276-279 NTTF

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

283-285 TDK

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 4

1 76-79 SSME
2 97-100 TPYE
3 215-218 SYED
4 297-300 SWED

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

92-99 RGNEDTPY

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

157-162 GLRLGG

[6] PDOC00009 PS00009 AMIDATION
Amidation site

122-125 NGRK

[7] PDOC00029 PS00029 LEUCINE_ZIPPER
Leucine zipper pattern

246-267 LAALNALLQWLLRPLVLYAPLL

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	6	26	0.633	Putative
2	237	257	1.571	Certain
3	260	280	0.819	Putative

FIGURE 2A

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BLAST Alignment to Top Hit:

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>CRA|335001098696094 /altid=gi|11545403
      /def=gb|AAG37824.1|AF277719_1 (AF277719) 3
      beta-hydroxy-delta 5-C27-steroid oxidoreductase [Homo
      sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa
      /length=369
      Length = 369

Score = 638 bits (1627), Expect = 0.0
Identities = 315/369 (85%), Positives = 316/369 (85%), Gaps = 52/369 (14%)

Query: 1  MADSAQAQKLVLVTGGCGFLGEHVVRMLLQREPRLGELRVFDQHLGPWLEELKTG---- 56
      MADSAQAQKLVLVTGGCGFLGEHVVRMLLQREPRLGELRVFDQHLGPWLEELKTG
Sbjct: 1  MADSAQAQKLVLVTGGCGFLGEHVVRMLLQREPRLGELRVFDQHLGPWLEELKTGPVRV 60

Query: 57  -----TRNVIEACVQTG 68
      TRNVIEACVQTG
Sbjct: 61  TAIQGDVTQAHEVAAVAGAHVVIHTAGLVDVFGRASPKTIHEVNVQGTRNVIEACVQTG 120

Query: 69  TRFLVYTSSMEVVGPNTKGHPFYRGNEPTPYEAVHRHPYPCKALAEWLVLEANGRKVRG 128
      TRFLVYTSSMEVVGPNTKGHPFYRGNEPTPYEAVHRHPYPCKALAEWLVLEANGRKVRG
Sbjct: 121 TRFLVYTSSMEVVGPNTKGHPFYRGNEPTPYEAVHRHPYPCKALAEWLVLEANGRKVRG 180

Query: 129 GLPLVTCALRPTGIYGEHGHQIMRDFYRQGLRLGGWLFRAIPASVEHGRVYVGNVAMMHVL 188
      GLPLVTCALRPTGIYGEHGHQIMRDFYRQGLRLGGWLFRAIPASVEHGRVYVGNVAMMHVL
Sbjct: 181 GLPLVTCALRPTGIYGEHGHQIMRDFYRQGLRLGGWLFRAIPASVEHGRVYVGNVAMMHVL 240

Query: 189 AARELEQRAALMGGQVYFCYDGSPPYRSYEDFNMEFLGPCGLRLVGARPLLPHYWLLVFLAA 248
      AARELEQRAALMGGQVYFCYDGSPP+RSYEDFNMEFLGPCGLRLVGARPLLPHYWLLVFLAA
Sbjct: 241 AARELEQRAALMGGQVYFCYDGSPPHRSYEDFNMEFLGPCGLRLVGARPLLPHYWLLVFLAA 300

Query: 249 LNALLQWLLRPLVLYAPLLNPYTLAVANTTFTVSTDKAQRHFGYEPLFSWEDSRTRTILW 308
      LNALLQWLLRPLVLYAPLLNPYTLAVAN TFTVSTDKAQRHFGYEPLFSWEDSRTRTILW
Sbjct: 301 LNALLQWLLRPLVLYAPLLNPYTLAVANATFTVSTDKAQRHFGYEPLFSWEDSRTRTILW 360

Query: 309 VQAATGSAQ 317
      VQAATGSAQ
Sbjct: 361 VQAATGSAQ 369 (SEQ ID NO: 4)
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Hammer search results (Pfam):

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
PF01073	3-beta hydroxysteroid dehydrogenase/isomeras	558.2	5.5e-164	2
PF01370	NAD dependent epimerase/dehydratase family	13.3	0.005	1
PF00438	S-adenosylmethionine synthetase	1.8	0.78	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF01370	1/1	12	31 ..	1	20 [.	13.3	0.005
PF01073	1/2	1	52 [.	1	53 [.	69.6	3.9e-18
PF00438	1/1	289	299 ..	365	376 .]	1.8	0.78
PF01073	2/2	55	313 ..	159	425 .]	489.6	2.4e-143

FIGURE 2B

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1  ATTTGCATTA GCCGGTGGCA GCCAACAGGT GCCTGTTTTG GAGAGAGGTC
51 CAGGGAGGAG AGATGAGCAG GGTGCCGTTG GTGACATGGC CAGTCATTTT
101 AGGAGCTGCC CCAACCCAG ACTTGCCCA GCAGTCCGGG ACCCCTGT
151 GACCAGGCAG ATGCTCGAAG GAGTCAGTGG CTCTCTTACC CAGTGCAGAT
201 TTCCCTGGAG TTCCCTGCGG GTGACTTAGA ATGGCCACCA GAGGCTTAGG
251 ATGCTGCCCC AAAGAGGGAG GGCTCCTGGA AGCAGAGTCG AGAGAGTCAG
301 TGCCGGGTTA GCGGGAGCTG GAGGCAGAGC TGCAGCTCCA GGCCTGGTGG
351 GCGTGGACCT GGGGTGCTGG CTGGCAGGCG TGCTCAGGGG CAGGAAGTGG
401 GGGACTCTTC CCTGACCATC GCATCTCACC CTGGCAGATG GTGGCCGACA
451 TGCGGGAGAA GCGCTACGTG CAGGAGGGCA TTGGCAGCAG CTACCTGTTC
501 CGGGTGGACC ACGACACCAT CATCGATGCC ACCAAGTGTG GCAACCTGGC
551 CAGATTTCATC AACCACTGCT GCACGGTGCG CCAGGGGGCA GCGGGGCGAG
601 GAGTTGGGGG TCGGTGGGGG TGGCCACGGC TCACACGCCC TTCCATCCGC
651 AGCCTAAGTG CTACGCCAAG GTCATCACC TCGAGTCCCA GAAGAAGATC
701 GTGATCTACT CCAAGCAGCC CATTGGCGTG GACGAGGAGA TCACCTACGA
751 CTACAAGTTC CCACTGGAAG ACAACAAGAT CCCGTGTCTG TGTGGCACAG
801 AGAGCTCCCG GGGCTCCCTA AACTGAGGTG GGGCAGGATG GGTGCCACA
851 CCCCTATTTA TTCCCTCTGG TGCCCTGAGC TCCAGCACC CCCCAGCCT
901 TAGTGGGCTC AGCAGGGGCC ACATGCCCC ATCTCCAAGC GTGGGGTTGG
951 GGGCCCCAAG CCCAGCGAGG GAGCCTCAGT CCCTGGAGGC AGCTTCTGCC
1001 TCTCCTGTCG CCCCTGCCCA CCACCCCTG ATTGTTTTTC TTTGCGGAGA
1051 AGAAGCTGTA AATGTTTTGT AGCAGCCAGC AGCTGTTTCC TGTGGAACC
1101 TGGGGTGCCG GCCTGTACAG ATTCTGTCTT GGGGGGCTAC ACAGTCTCTT
1151 CGCTTTGTGT TAATGGGGAC TTCCCTTTAC GCCCTGCGTG TACCCCTCCC
1201 CAGTTTAGGG GTCTCTGGGG CAGTGGCCAT GTTCTCCCC TGGGGGGGCT
1251 CTGCACCCCC AGTCTGGGG ACTCCGTGCC TGGAACCCCT CCTCATCTGT
1301 TCCTGCCAGA CCCTGAGGGT CACCCTTCCA CCCTGGTGTG ACTCCCCGGC
1351 TCAGCCAGGC CAGGATGGCG GGGTGGGTCC CTTTGTCTGG GCTGGACTGT
1401 ACATATGTTA ATAGCGCAAA CCCGACGCCA CATTTTTATA ATTGTGATTA
1451 AACTTTATTG TACAAAAGTG TTTGGTGGT GTATTTGGGC AGGAGCGAGG
1501 GGTGGGGGGT AGAGGGCAGC GAGGGTTGTG CAAGTTGAAG AGAGGAAAA
1551 GTGGGTACCT GAAGTGTGGG GCAGGTAAAG GGGCCTTCAG GCAAGAGCCC
1601 AGACCTGCAG AGACAGTCCG AGACTGTCTC GGACCCCTG ACAGGCTGCA
1651 GCAGCCGCAC CCGCACCAGG AATACCCAC CAGTGCCCGC CAGGGTGGTG
1701 CCAAGGTCAG GCCTCCCTTT CCTACAATCA CAGCTGCAGC TGGACCTCCG
1751 GCCTCCTGGG AAGCCAGCA GGAGGGAAGG CCTGAGGTCA CACTGTGGGA
1801 TGAGGTCACC GCTGGCTCCA CCCACAGCCC CAGACCCCTT CAGCCACTC
1851 TGCAAGTTCG AGCTTCATCC CCACCAAGTT CTCCGCTGGA CCCAGATGCC
1901 AGTGGAGCAC AGAGCGGCCG CCAGGGGGCG CCTTGGGGCA AGAGTGGTGG
1951 GGGTTGTGGC TGGGCGGGTC TCTGTTCTTG GAATGGGGCA GGAGGGAGAA
2001 GGAGGAGCCA GCGGAAGGAC GGTGTGCGGG CCGGCCAGCC CTGGACGAAA
2051 GAAGAGGGCC CCTCCAGGCC AGTCTGGGCA CCCTGGGATA GCGGCTGCAG
2101 GTAGGCAGAG GCGCTGCCAG TGCCAGGTG GCCTTTCCCT CCATCCGGCC
2151 CTTCCCACTT TCCTATAACC TTCCCTCAC CTCCCTCAAC TCCTGGCCTC
2201 CCCACCCCTT TACTGCCTTC AAATCTCTCT CCCTAAACCC TGACCCCTTC
2251 CTGCACCCCA AGCCCGCCCC TCTCTCCGTA ACTCAGCCAT CAGCAGGGGC
2301 AGACGGCAGG TGGCTGGTGT GCTGCAGCTC CCAGGATCAG CTCTGCCCTC
2351 CCGCCAAACG CCAGCCTCGT CACCGCTCCA GGGCACCTCC AGCAGTAACA
2401 GGTGGTTGCA GCAGGTGGCA GCCAGCCCCT GGATGAGCCA AGGTCTCTTC
2451 CCCAGCCAGG CATGGCCGAC TCTGCACAGG CCCAGAAGCT GGTGTACCTG
2501 GTCACAGGGG GCTGTGGCTT CCTGGGAGAG CACGTGGTGC GAATGCTGCT
2551 GCAGCGGGAG CCCCAGCTCG GGGAGCTGCG GGTCTTTGAC CAACACCTGG
2601 GTCCCTGGCT GGAGGAGCTG AAGACAGGTT CTTGTTGGGG GAGCTTGTGG
2651 TGGAGAGGGT GTGGACGCTT CCCCAACCCT TCCCAAGCTG GGATCCCCAC
2701 CCTGTCAGTG GAACAGATGA TGCTGGTTTC TGTCCACATG GATGGGTCTG
2751 GTGAGTCACA TTGGGAACGT GACTCCAGGG TGGAAGATGA ACCCAGCCTC
2801 TGGCCTCTGG CCCCAGCTCT GACATGGCCT GTGTCCTCCA ACCCCGGCCA
2851 GGGCCTGTGA GGGTGAAGTC CATCCAGGGG GACGTGACCC AGGCCATGA
2901 GGTGGCAGCA GCTGTGGCCG GAGCCCATGT GGTCTATCCAC ACGGCTGGGC
2951 TGGTAGACGT GTTTGGCAGG GCCAGTCCCA AGACCATCCA TGAGGTCAAC
3001 GTGCAGGGTG AGGAGCTCTG GACACTCCTG GCCATCTTGC CTGTTTGTTC
3051 CCCACTCTGT CTTTGGCCTT GACCTCCGGT GACTCCCTG GGACAAGTTG

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FIGURE 3A

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3101	TCCTATTGAC	AGCCCTGCC	CCGCCTCCCC	TGACCTGTCA	TGGTTTTCCC
3151	TGGACCTGGG	ATGGGGAGGA	GGAGATGCA	GAGAGGGAAG	AAGCTGCAGC
3201	TTGGATACGC	CTCCTCCTCT	GCCAGGTACC	CGGAACGTGA	TCGAGGCTTG
3251	TGTGCAGACC	GGAACACGGT	TCCTGGTCTA	CACCAGCAGC	ATGGAAGTTG
3301	TGGGGCCTAA	CACCAAAGGT	CACCCCTTCT	ACAGGTGAGT	GGCAGGCCCT
3351	CTTGTCTCT	AAGAGCCCAT	TTCCTCAGC	ATTGAGTCTT	CCTTCTCCTC
3401	CCACCAGGGG	CAACGAAGAC	ACCCCATACG	AAGCAGTGCA	CAGGCACCCC
3451	TATCCTTGCA	GCAAGGCCCT	GGCCGAGTGG	CTGGTCCTGG	AGGCCAACGG
3501	GAGGAAGGTG	AGCCCAAGAA	AAGGAGGCGC	AGAGATGGGG	CTCCTGCCCT
3551	GCACACCCCC	TTACCCTGCC	AGCCCAAGGA	GGCCGGGGCC	GAGAGCAAGC
3601	TGTGGGTGCC	CAGGTCTCAG	CAGTACCTGC	CTTTGCCACC	AGGTCCGTGG
3651	GGGGCTGCC	CTGGTGACGT	GTGCCCTTCG	TCCACGCGG	ATCTACGGTG
3701	AAGGCCACCA	GATCATGAGG	GACTTCTACC	GCCAGGGCCT	GCGCCTGGGA
3751	GTTTGGCTCT	TCCGGGCCAT	CCCGCCTCT	GTGGAGCATG	GCCGGGTCTA
3801	TGTGGGTGAG	GACTGGGCTA	GGCAGGGGGA	GGCTGAGAAT	ATGGCAGGAG
3851	GACTTGCTCT	AGAAGGGGGC	AGGACCCACA	TGGCCCTGGG	AGAGAAGTGT
3901	GGACTCTGGC	TAGAAAAATA	TGGTCTATAC	ATGGGCCAAG	GTAGACTGTG
3951	ATTATGTCTC	CACAGCCTGC	AGAGAATACA	GGATCCATGC	AAGTTGGGAC
4001	ATTAAAAAGT	GTATCATAGG	CTACAGAGAA	GATTGCAGCT	ATGGGAGCAG
4051	CCATTCCCA	GGAGAGGAGA	GGAGAGGGAC	AGTGTGTACA	CAGCACTAAA
4101	AGGGCTGGGT	TCAGTGGCTC	GCATCTATAA	TCCAGCACT	TTAGGAGGCT
4151	GAGGCGGGAG	GATGGCCTGA	GCCCAGGAGT	TGGAGGCTGC	AGTGAGCTAT
4201	GACCGCACCA	CTGCACTCCA	GCCTGGATGA	CAGAGACAGA	CCCTGTCTCT
4251	AAAACTTTTT	TTAAAGGAAG	TAGCATCTAC	ACAGGGAATA	AGGTCACCTG
4301	CCACTCCATC	CTGCAGTCCC	CAAGCCTCTC	AGGGCCCACC	ACGCAGGTCC
4351	TGGTTTCTCT	ATCCTCTCCC	CAGGTTCTTT	GCAGATGCAG	GCTGGCCAG
4401	GAGAGCAAGT	GACTACCAGG	GCGAGGGAGA	AGGCAGCCTT	TCCCAGGCTG
4451	CTGTGGGGAT	GTGGGCGGCA	ACTACCTGGG	CCCAAAGAGG	GGGTGGCCCA
4501	GGAGAGCAGC	CTCGATGTGG	TGTTGCAAGG	GCACTCAGGG	GTGTGTCCGC
4551	CTCTCTTCCG	CCACCGGCAG	GCAATGTTGC	CTGGATGCAC	GTGCTGGCAG
4601	CCCGGGAGCT	GGAGCAGCGG	GCAGCCCTGA	TGGGCGGCCA	GGTATACTTC
4651	TGCTACGATG	GATCACCCCTA	CAGGAGCTAC	GAGGATTTC	ACATGGAGTT
4701	CCTGGGCCCC	TGCGGACTGC	GGCTGGTGGG	CGCCCGCCCA	TTGCTGCCCT
4751	ACTGGCTGCT	GGTGTTCCTG	GCTGCCCTCA	ATGCCCTGCT	GCAGTGGCTG
4801	CTGCGGCCAC	TGGTGTCTTA	CGCACCCCTG	CTGAACCCCT	ACACGCTGGC
4851	CGTGGCCAA	ACCACCTTCA	CCGTACAGC	CGACAAGGCT	CAGCGCCATT
4901	TCGGCTATGA	GCCCCGTTC	TCGTGGGAGG	ATAGCCGGAC	CCGCACCAT
4951	CTCTGGGTAC	AGGCCGCTAC	GGGTTAGGCC	CAGTGACGGT	GGGGCTGGGG
5001	CCTGGAGGCC	CAGATACAGC	ACATCCACCC	AGGTCCCAG	CCCTCACACC
5051	CTGGACGGGA	AGGGACAGCT	GCATTCCAGA	GCAGGAGGCA	GGGCTTCTGG
5101	GGCCAGAATG	GCTGTCTTTG	TGCTAGAGCC	CTCCACATTT	TCTTTTTCTT
5151	TTTTGAGACA	GGGTCTTGCT	CTGTACCCCA	GACTGGAGTG	CAGTGGTGTG
5201	ATCATAGCTC	ACTGCACCTC	CAACCTCCTG	GTTTCAAGCA	ATCTCCTG
5251	CTCAGCCTCC	TTGAACAGCT	GGGACCAAC	GTGCACGCCA	CCACACCTGG
5301	CTTTTTTTTG	TTGTTTTTAG	AGACAGGGTC	TCACTATATT	GCTCAGGCTG
5351	GTCTTGAAC	CCTGGGCTCA	AGTGATCTTC	CCACGTGGGC	CTCCAAAAC
5401	GCTGGAAC	CAAGTGTGAG	CCACCGCGCC	TGGCCCAAGC	CCTCCACATT
5451	TTCAATCCAG	GAGCCTTGAG	TCTGTGTTGT	GTCCTGACAC	CTCCAAGTTC
5501	TAGGGCCGTC	AGGACACGGG	AGGGTTTGGG	GACAGAGTGT	CCTTCTCTG
5551	TCCTCTCATC	CCAGTCCTGA	TGGCCGCTTG	GTGAGTGTCT	GGTGCCCTGG
5601	TGGCCTGCCC	CAGCTCTCTT	CTGGCTTTCT	GAGCAGGAAG	CGAGCAGAGG
5651	CTCCACAGGC	TTACGCTGCT	CTCCTGACAG	CCACACGCGA	CCCTCGGTGC
5701	AGAGTGACAG	GGCGGCTCTG	GTTCTCCAG	CCACCTCAGT	CCCTCTTTGG
5751	GAGGTGATGT	TCCCATTGTT	TTTCAAAGGC	CTACCTTCA	ACTGTCTGTC
5801	TTAGAATTCC	CCTCTGGAGG	GCTATGGCCT	CCCTATGCTT	TCACTTCCCA
5851	CCTCTCTACC	TAAGTTCCTT	CCCAGCACAT	CGCCAGCCCT	GGGCCTGGGG
5901	ATGTCCCCAA	TGCTGTACCT	GGCTGACCCC	GGATTAAAAG	CCTCATCCAC
5951	GACCGTGTCC	ATCTGTCTGT	CCAGCTCTCC	CTCCCATCCC	CCCACCCCAT
6001	GTCCGCCTCC	CCACGCGGCC	CATCCACAGT	GGGGACAGAA	GGAAGTGAGC
6051	ACACGGCACA	CCCGCTGTTG	GATTGGTTGC	TATTTCTCCC	GTCCACAGG
6101	GCCTGACCTG	GCCCAGGGTG	GGGTGGGGGG	CTCTGGGGAC	AGGACATGCA
6151	GGGAGGAAGG	GGGGGACAGG	ATTTTCCTGT	GTTTATCCA	TTTGCAAGTT

FIGURE 3B

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6201 GGTACCAAT AGAAATGGGA CTCTGAGGGC TAACAGAAAT GGGACTCTGA
6251 GGGCTAACAG GAGAGGGCGG CCTGGCTCTG GGCCCCAGCC AGGCCCCAGG
6301 AGTCCTGTCC CCTCTGAGAA GGGGAGGGAG AGAGCTCTAG AAACCAACGG
6351 AGAAACAGAG AAGGGGGCAG GGGCTCATGT CAGCAAACAC GGCTACATCA
6401 CGTGACACGC CAGTGACACA GAAACACACG CCAACGCACA CGGCTGCACA
6451 GCGGGCAGGG GCGGTTAGGG GAAAGGGAGC CGGGGCCACC CATCTTGTC
6501 TCTGCAGGGC GGGCTGGGGG GCAGGGTGAA TGCATAGAAC ACATCATGTG
6551 TACACGCTCA GGGCGTGGCA AGAGCGTGCG TCGACCCACG GGTACATGGG
6601 ATGGACACGC AGTGTGCTTC ATGAGGGGTG GGAACAGGGA GGAGGGGGAA
6651 GAGGAAGCAC TGAGCCCTGG CCAGGCCCCG GACCACCCGC AGGGCACACG
6701 TGGGGCACAT GTGGGCTCAA TGGTTGCAGG CGCCTGGGCA GGTAGCACAC
6751 ATTTGTCCAA GAACATGCAA AAGACACCAG CCTCCAGACA ACATGCCAGG
6801 ACGCACACAG ACAGCAGCCA ACAAGCAGGC ACATCATAGG ATGTGGAGGA
6851 CGCATAGAAA GGGCACAGCA GACCCTTAGA GATCCCCTGG TCCACCTGAG
6901 GCCCAGAGAT GGGCAGCTGT GGGCCCAATG CCACTCCAGG TGGGGGGAGT
6951 GGTGCCCCAG CCACTGCTCA ACCCTTCTCC TGTGGCCCCA AGGCCGTGGG
7001 ACTTCCGAAA ACACCTGGGC TGAATGGGGG TCCTGTCCAG GCGGCCGAA
7051 GAGGGGACTG GGGGTGGGG CCTGCTCTGA TGTCTCCAA GCAGCCCAG
7101 ATGGGAGCAG GAGGGCCGTG GCCAGACTTG GGGCAGACTT CCTGTCCTGC
7151 AGAGGGGCGT TCTGGGAAGG GACAGGCAGG CCCCAGCTC AGGACAGCCC
7201 ACCTGGGGTT ACGCACGTGG CCACACTGAC ACACACACAG GACAAGGGAG
7251 AGCTCGGCTG TCTGAGCTCG GGTAGAGGTG GAGGGGTACT GTGTTCTGGG
7301 A

```

(SEQ ID NO: 3)

FEATURES:

Start: 2462
Exon: 2462-2627
Intron: 2628-3225
Exon: 3226-3334
Intron: 3335-3407
Exon: 3408-3507
Intron: 3508-3642
Exon: 3643-3805
Intron: 3806-4570
Exon: 4571-4983
Stop: 4984

SNPs:

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
1010	A	G	Beyond ORF(5')			
1151	C	T	Beyond ORF(5')			
4805	G	A	Exon	258	R	Q
6293	G	A	Beyond ORF(3')			

Context:

DNA
Position

```

1010 TCCAAGCAGCCCATTTGGCGTGGACGAGGAGATCACCTACGACTACAAGTTCCCACTGGAA
GACAAACAAGATCCCGTGTCTGTGTGGCACAGAGAGCTGCCGGGGCTCCCTAAACTGAGGT
GGGGCAGGATGGGTGCCACACCCCTATTTATTTCCCCTGGTGCCTGAGCTCCCAGCAC
CCCCCAGCCTTAGTGGGCTCAGCAGGGCCACATGCCCCATCTCCAAGCGTGGGGTTG
GGGGCCCAAGCCAGCGAGGGAGCCTCAGTCCCTGGAGGCAGCTTCTGCCTCTCCTGTC
[A,G]
CCCCTGCCCAACCACCCCTGATTGTTTTTCTTTGCGGAGAAGAAGCTGTAAATGTTTTGT
AGCAGCCAGCAGCTGTTTCTGTGGAAACCTGGGGTGCCGCGCTGTACAGATTCTGTCT

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FIGURE 3C

Docket No. CL001181DIV2
Serial No. To Be Assigned
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEINS...

GGGGGGCTACACAGTCCTCTCGCTTTGTGTTAATGGGGACTTCCCCCTTACGCCCTGCGTG
TACCCCTCCCCAGTTTAGGGGTCTCTGGGGCAGTGGCCATGTTCTCCCCCTGGGGGGGT
CTGCAACCCAGTCCTGGGGACTCCGTGCTGGAACCTGECTCATCTGTTCTGCCAGA

1151 CCCCTATTTATCCCCCTGGTGCCCTGAGCTCCCAGCACCCCCCAGCCTTAGTGGGCTC
AGCAGGGCCCATGCCCCCATCTCCAAGCGTGGGGTGGGGGGCCCAAGCCAGCGAGG
GAGCCTCAGTCCCTGGAGGCAGCTTCTGCCTCTCCTGTGCCCCCTGCCACCACCCCTG
ATTGTTTTTCTTTGCGGAGAAGAAGCTGTAAATGTTTTGTAGCAGCCAGCAGCTGTTCC
TGTGGAAACCTGGGGTGCCGGCCTGTACAGATTCTGTCTGGGGGGCTACACAGTCCTCT
[C, T]
GCTTTGTGTTAATGGGGACTTCCCCCTTACGCCCTGCGTGTACCCCTCCCCAGTTTAGGG
TCTCTGGGGCAGTGGCCATGTTCTCCCCCTGGGGGGGTCTGACCCCCAGTCTCGGGGA
CTCCGTGCCTGGAACCTGCCTCATCTGTTCTGCCAGACCCTGAGGGTACCCTTCCAC
CCTGGTGTACTCCCCGGCTCAGCCAGGCCAGGATGGCGGGTGGGTCCCTTTTGCTGGG
CTGGACTGTACATATGTTAATAGCGCAAACCCGACGCCACATTTTATAATTGTGATTAA

4805 AGCAGCCTCGATGTGGTGTGCAAGGGCACTCAGGGGTGTGTCCGCCTCTCTTCCGCCAC
CGGCAGGCAATGTTGCCTGGATGCACGTGCTGGCAGCCCGGAGCTGGAGCAGCGGGCAG
CCCTGATGGGCGGCCAGGTATACTTCTGCTACGATGGATCACCTACAGGAGCTACGAGG
ATTTCAACATGGAGTTCTTGGGCCCCTGCGACTGCGGTGGTGGGCGCCCGCCATTGC
TGCCCTACTGGCTGCTGGTGTCTCTGGCTGCCCTCAATGCCCTGCTGCAGTGGCTGCTGC
[G, A]
GCCACTGGTGTCTTACGCACCCCTGCTGAACCCCTACACGCTGGCCGTGGCCAACACCAC
CTTCACCGTCAGCACCGACAAGGCTCAGCGCCATTTCTGGCTATGAGCCCTGTTCTCGTG
GGAGGATAGCCGGACCCGACCATTTCTTGGGTACAGGCCGCTACGGGTTCAGCCCACTG
ACGGTGGGGCTGGGGCCTGGAGGCCAGATACAGCACATCCACCCAGGTCCCGAGCCCTC
ACACCCCTGGACGGGAAGGGACAGCTGCATTCAGAGCAGGAGGCAGGGCTTCTGGGGCCA

6293 CACCCCATGTCCGCCTCCCCACGGCGCCCATCCCACGTGGGGACAGAAGGAAGTGAGCAC
ACGCACACCCGCTGTTGGATTGGTTGCTATTTCTCCCGTCCCACAGGGCCTGACCTGGC
CCAGGGTGGGGTGGGGGGCTCTGGGGACAGGACATGCAGGGAGGAAGGGGGGGCAGGAT
TTTCTGTGTTTTATCCATTGCAAGTTGGTCACCAATAGAAATGGGACTCTGAGGGCTA
ACAGAAATGGGACTCTGAGGGCTAACAGGAGAGGGCGGCCTGGCTCTGGGCCCCAGCCAG
[G, A]
CCCCAGGAGTCCTGTCCCCTCTGAGAAGGGGAGGGAGAGAGCTCTAGAAACCAACGGAGA
AACAGAGAAGGGGGCAGGGGCTCATGTCAGCAAACACGGCTACATCACGTGACACGCCAG
TGACACAGAAACACACGCCAACGCACACGGCTGCACAGCGGGCAGGGGCGGTTAGGGGAA
AGGGAGCCGGGGCCACCATCTTGTCTCTGCAGGGCGGGCTGGGGGGCAGGGTGAATGC
ATAGAACACATCATGTGTACAGCTCAGGGCGTGGCAAGAGCGTGCCTCGACCCACGGT

Chromosome map:
Chromosome 12